

SEQUENCE LISTING

<110> Yang, Meija

<120> NOVEL THERAPEUTIC FUSION PROTEINS

<130> ARS-121

<140> US 10/566,929

<141> 2006-02-02

<150> US 60/492,397

<151> 2003-08-04

<160> 24

<170> PatentIn version 3.1

<210> 1

<211> 183

<212> PRT

<213> Homo sapiens

<400> 1

Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu Phe Met Gly Ala Ser
1 5 10 15

Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp
20 25 30

Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser Arg Arg Val Glu Pro
35 40 45

Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp Leu Gln
50 55 60

Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val Asp Phe
65 70 75 80

Trp Thr Ile Met Glu Asn His Asn His Ser Lys Glu Ser His Thr Leu
85 90 95

Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr Glu Gly
100 105 110

Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His Leu Glu Phe Cys Pro
115 120 125

Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro Thr Lys
130 135 140

Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg Ala Tyr
145 150 155 160

Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln Leu Leu Glu Leu Gly
 165 170 175

Arg Gly Val Leu Asp Gln Gln
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<210> 2
 <211> 661
 <212> PRT
 <213> Homo sapiens

<400> 2

Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile
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Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly
 20 25 30

Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala
 35 40 45

Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala
 50 55 60

Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln
 65 70 75 80

Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn
 85 90 95

Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro
 100 105 110

Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val
 115 120 125

Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala
 130 135 140

Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe
 145 150 155 160

Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val
 165 170 175

Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala
 180 185 190

Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro
 195 200 205

Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala

210	215	220
Val Val Ala Arg Ser	Val Asn Gly Lys Glu Asp	Ala Ile Trp Asn Leu
225	230	235 240
Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe	245	250 255
Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp	260	265 270
Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu	275	280 285
Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser	290	295 300
Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val	305	310 315 320
Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu	325	330 335
Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala	340	345 350
Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr	355	360 365
Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn	370	375 380
Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg	385	390 395 400
Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr	405	410 415
Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala	420	425 430
Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn	435	440 445
Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala	450	455 460
Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp	465	470 475 480
Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr	485	490 495
Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val	500	505 510

Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn
 515 520 525

Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu
 530 535 540

Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His
 545 550 555 560

Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val
 565 570 575

Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg
 580 585 590

Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr
 595 600 605

Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His
 610 615 620

Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly
 625 630 635 640

Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys
 645 650 655

Glu Phe Leu Arg Lys
 660

<210> 3
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 3

Val Pro Pro Leu Val Lys Val Thr His His Val Thr Ser Ser Val Thr
 1 5 10 15

Thr Leu Arg Cys Arg Ala Leu Asn Tyr Tyr Pro Gln Asn Ile Thr Met
 20 25 30

Lys Trp Leu Lys Asp Lys Gln Pro Met Asp Ala Lys Glu Phe Glu Pro
 35 40 45

Lys Asp Val Leu Pro Asn Gly Asp Gly Thr Tyr Gln Gly Trp Ile Thr
 50 55 60

Leu Ala Val Pro Pro Gly Glu Glu Gln Arg Tyr Thr Cys Gln Val Glu
 65 70 75 80

His Pro Gly Leu Asp Gln Pro Leu Ile Val Ile Trp

85

90

<210> 4
 <211> 753
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 <213> Artificial sequence

<220>

<223> Lactoferrin / HFE-based recycling domain RC1

<400> 4

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Gln	Ala	Ile	Ala	Glu	Asn	Arg	Ala	Asp	Ala	Val	Thr	Leu	Asp	Gly	Gly	20	25	30	
Phe	Ile	Tyr	Glu	Ala	Gly	Leu	Ala	Pro	Tyr	Lys	Leu	Arg	Pro	Val	Ala	35	40	45	
Ala	Glu	Val	Tyr	Gly	Thr	Glu	Arg	Gln	Pro	Arg	Thr	His	Tyr	Tyr	Ala	50	55	60	
Val	Ala	Val	Val	Lys	Lys	Gly	Gly	Ser	Phe	Gln	Leu	Asn	Glu	Leu	Gln	65	70	75	80
Gly	Leu	Lys	Ser	Cys	His	Thr	Gly	Leu	Arg	Arg	Thr	Ala	Gly	Trp	Asn	85	90	95	
Val	Pro	Ile	Gly	Thr	Leu	Arg	Pro	Phe	Leu	Asn	Trp	Thr	Gly	Pro	Pro	100	105	110	
Glu	Pro	Ile	Glu	Ala	Ala	Val	Ala	Arg	Phe	Phe	Ser	Ala	Ser	Cys	Val	115	120	125	
Pro	Gly	Ala	Asp	Lys	Gly	Gln	Phe	Pro	Asn	Leu	Cys	Arg	Leu	Cys	Ala	130	135	140	
Gly	Thr	Gly	Glu	Asn	Lys	Cys	Ala	Phe	Ser	Ser	Gln	Glu	Pro	Tyr	Phe	145	150	155	160
Ser	Tyr	Ser	Gly	Ala	Phe	Lys	Cys	Leu	Arg	Asp	Gly	Ala	Gly	Asp	Val	165	170	175	
Ala	Phe	Ile	Arg	Glu	Ser	Thr	Val	Phe	Glu	Asp	Leu	Ser	Asp	Glu	Ala	180	185	190	
Glu	Arg	Asp	Glu	Tyr	Glu	Leu	Leu	Cys	Pro	Asp	Asn	Thr	Arg	Lys	Pro	195	200	205	
Val	Asp	Lys	Phe	Lys	Asp	Cys	His	Leu	Ala	Arg	Val	Pro	Ser	His	Ala	210	215	220	

Val	Val	Ala	Arg	Ser	Val	Asn	Gly	Lys	Glu	Asp	Ala	Ile	Trp	Asn	Leu	225	230	235	240
Leu	Arg	Gln	Ala	Gln	Glu	Lys	Phe	Gly	Lys	Asp	Lys	Ser	Pro	Lys	Phe	245	250	255	
Gln	Leu	Phe	Gly	Ser	Pro	Ser	Gly	Gln	Lys	Asp	Leu	Leu	Phe	Lys	Asp	260	265	270	
Ser	Ala	Ile	Gly	Phe	Ser	Arg	Val	Pro	Pro	Arg	Ile	Asp	Ser	Gly	Leu	275	280	285	
Tyr	Leu	Gly	Ser	Gly	Tyr	Phe	Thr	Ala	Ile	Gln	Asn	Leu	Arg	Lys	Ser	290	295	300	
Glu	Glu	Glu	Val	Ala	Ala	Arg	Arg	Ala	Arg	Val	Val	Trp	Cys	Ala	Val	305	310	315	320
Gly	Glu	Gln	Glu	Leu	Arg	Lys	Cys	Asn	Gln	Trp	Ser	Gly	Leu	Ser	Glu	325	330	335	
Gly	Ser	Val	Thr	Cys	Ser	Ser	Ala	Ser	Thr	Thr	Glu	Asp	Cys	Ile	Ala	340	345	350	
Leu	Val	Leu	Lys	Gly	Glu	Ala	Asp	Ala	Met	Ser	Leu	Asp	Gly	Gly	Tyr	355	360	365	
Val	Tyr	Thr	Ala	Gly	Lys	Cys	Gly	Leu	Val	Pro	Val	Leu	Ala	Glu	Asn	370	375	380	
Tyr	Lys	Ser	Gln	Gln	Ser	Ser	Asp	Pro	Asp	Pro	Asn	Cys	Val	Asp	Arg	385	390	395	400
Pro	Val	Glu	Gly	Tyr	Leu	Ala	Val	Ala	Val	Val	Arg	Arg	Ser	Asp	Thr	405	410	415	
Ser	Leu	Thr	Trp	Asn	Ser	Val	Lys	Gly	Lys	Lys	Ser	Cys	His	Thr	Ala	420	425	430	
Val	Asp	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met	Gly	Leu	Leu	Phe	Asn	435	440	445	
Gln	Thr	Gly	Ser	Cys	Lys	Phe	Asp	Glu	Tyr	Phe	Ser	Gln	Ser	Cys	Ala	450	455	460	
Pro	Gly	Ser	Asp	Pro	Arg	Ser	Asn	Leu	Cys	Ala	Leu	Cys	Ile	Gly	Asp	465	470	475	480
Glu	Gln	Gly	Glu	Asn	Lys	Cys	Val	Pro	Asn	Ser	Asn	Glu	Arg	Tyr	Tyr	485	490	495	
Gly	Tyr	Thr	Gly	Ala	Phe	Arg	Cys	Leu	Ala	Glu	Asn	Ala	Gly	Asp	Val	500	505	510	
Ala	Phe	Val	Lys	Asp	Val	Thr	Val	Leu	Gln	Asn	Thr	Asp	Gly	Asn	Asn				

515					520					525					
Asn	Glu	Ala	Trp	Ala	Lys	Asp	Leu	Lys	Leu	Ala	Asp	Phe	Ala	Leu	Leu
530						535					540				
Cys	Leu	Asp	Gly	Lys	Arg	Lys	Pro	Val	Thr	Glu	Ala	Arg	Ser	Cys	His
545					550					555					560
Leu	Ala	Met	Ala	Pro	Asn	His	Ala	Val	Val	Ser	Arg	Met	Asp	Lys	Val
				565					570					575	
Glu	Arg	Leu	Lys	Gln	Val	Leu	Leu	His	Gln	Gln	Ala	Lys	Phe	Gly	Arg
			580					585					590		
Asn	Gly	Ser	Asp	Cys	Pro	Asp	Lys	Phe	Cys	Leu	Phe	Gln	Ser	Glu	Thr
		595					600					605			
Lys	Asn	Leu	Leu	Phe	Asn	Asp	Asn	Thr	Glu	Cys	Leu	Ala	Arg	Leu	His
	610					615					620				
Gly	Lys	Thr	Thr	Tyr	Glu	Lys	Tyr	Leu	Gly	Pro	Gln	Tyr	Val	Ala	Gly
625					630					635					640
Ile	Thr	Asn	Leu	Lys	Lys	Cys	Ser	Thr	Ser	Pro	Leu	Leu	Glu	Ala	Cys
				645					650					655	
Glu	Phe	Leu	Arg	Lys	Val	Pro	Pro	Leu	Val	Lys	Val	Thr	His	His	Val
			660					665					670		
Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala	Leu	Asn	Tyr	Tyr	Pro
		675					680					685			
Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys	Gln	Pro	Met	Asp	Ala
	690					695					700				
Lys	Glu	Phe	Glu	Pro	Lys	Asp	Val	Leu	Pro	Asn	Gly	Asp	Gly	Thr	Tyr
705					710					715					720
Gln	Gly	Trp	Ile	Thr	Leu	Ala	Val	Pro	Pro	Gly	Glu	Glu	Gln	Arg	Tyr
				725					730					735	
Thr	Cys	Gln	Val	Glu	His	Pro	Gly	Leu	Asp	Gln	Pro	Leu	Ile	Val	Ile
			740					745					750		

Trp

<210> 5
 <211> 275
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Lactoferin / HFE-based recycling domain RC2

<400> 5

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 Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp
 20 25 30
 Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser Arg Arg Val Glu Pro
 35 40 45
 Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp Leu Gln
 50 55 60
 Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val Asp Phe
 65 70 75 80
 Trp Thr Ile Met Glu Asn His Asn His Ser Lys Glu Ser His Thr Leu
 85 90 95
 Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr Glu Gly
 100 105 110
 Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His Leu Glu Phe Cys Pro
 115 120 125
 Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro Thr Lys
 130 135 140
 Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg Ala Tyr
 145 150 155 160
 Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln Leu Leu Glu Leu Gly
 165 170 175
 Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu Val Lys Val Thr His
 180 185 190
 His Val Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr
 195 200 205
 Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met
 210 215 220
 Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly
 225 230 235 240
 Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu Glu Gln
 245 250 255
 Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro Leu Ile
 260 265 270
 Val Ile Trp
 275


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<220>
<223>  Lactoferrin / HFE-based recycling domain RC3
<400>  6
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Val 1	Pro	Pro	Leu	Val 5	Lys	Val	Thr	His	His 10	Val	Thr	Ser	Ser	Val 15	Thr
Thr	Leu	Arg	Cys 20	Arg	Ala	Leu	Asn	Tyr 25	Tyr	Pro	Gln	Asn	Ile 30	Thr	Met
Lys	Trp	Leu	Lys 35	Asp	Lys	Gln	Pro	Met 40	Asp	Ala	Lys	Glu 45	Phe	Glu	Pro
Lys	Asp 50	Val	Leu	Pro	Asn	Gly 55	Asp	Gly	Thr	Tyr	Gln 60	Gly	Trp	Ile	Thr
Leu 65	Ala	Val	Pro	Pro	Gly 70	Glu	Glu	Gln	Arg	Tyr 75	Thr	Cys	Gln	Val	Glu 80
His	Pro	Gly	Leu	Asp 85	Gln	Pro	Leu	Ile	Val 90	Ile	Trp	Gly	Pro	Pro 95	Val
Ser	Cys	Ile	Lys 100	Arg	Asp	Ser	Pro	Ile 105	Gln	Cys	Ile	Gln	Ala 110	Ile	Ala
Glu	Asn	Arg 115	Ala	Asp	Ala	Val	Thr 120	Leu	Asp	Gly	Gly	Phe 125	Ile	Tyr	Glu
Ala	Gly 130	Leu	Ala	Pro	Tyr	Lys 135	Leu	Arg	Pro	Val	Ala 140	Ala	Glu	Val	Tyr
Gly 145	Thr	Glu	Arg	Gln	Pro 150	Arg	Thr	His	Tyr	Tyr 155	Ala	Val	Ala	Val	Val 160
Lys	Lys	Gly	Gly	Ser 165	Phe	Gln	Leu	Asn	Glu 170	Leu	Gln	Gly	Leu	Lys 175	Ser
Cys	His	Thr	Gly 180	Leu	Arg	Arg	Thr	Ala 185	Gly	Trp	Asn	Val	Pro 190	Ile	Gly
Thr	Leu	Arg 195	Pro	Phe	Leu	Asn	Trp 200	Thr	Gly	Pro	Pro	Glu 205	Pro	Ile	Glu
Ala	Ala 210	Val	Ala	Arg	Phe	Phe 215	Ser	Ala	Ser	Cys	Val 220	Pro	Gly	Ala	Asp
Lys	Gly	Gln	Phe	Pro	Asn	Leu	Cys	Arg	Leu	Cys	Ala	Gly	Thr	Gly	Glu

225		230		235		240
Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe Ser Tyr Ser Gly						
		245		250		255
Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val Ala Phe Ile Arg						
		260		265		270
Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala Glu Arg Asp Glu						
		275		280		285
Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro Val Asp Lys Phe						
		290		295		300
Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala Val Val Ala Arg						
		305		310		315
Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu Leu Arg Gln Ala						
		325		330		335
Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe Gln Leu Phe Gly						
		340		345		350
Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp Ser Ala Ile Gly						
		355		360		365
Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu Tyr Leu Gly Ser						
		370		375		380
Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser Glu Glu Glu Val						
		385		390		395
Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val Gly Glu Gln Glu						
		405		410		415
Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu Gly Ser Val Thr						
		420		425		430
Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala Leu Val Leu Lys						
		435		440		445
Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr Val Tyr Thr Ala						
		450		455		460
Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Lys Ser Gln						
		465		470		475
Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg Pro Val Glu Gly						
		485		490		495
Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr Ser Leu Thr Trp						
		500		505		510
Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala Val Asp Arg Thr						
		515		520		525

Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn Gln Thr Gly Ser
 530 535 540
 Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala Pro Gly Ser Asp
 545 550 555 560
 Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp Glu Gln Gly Glu
 565 570 575
 Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr Gly Tyr Thr Gly
 580 585 590
 Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val Ala Phe Val Lys
 595 600 605
 Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn Asn Glu Ala Trp
 610 615 620
 Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu Cys Leu Asp Gly
 625 630 635 640
 Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His Leu Ala Met Ala
 645 650 655
 Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val Glu Arg Leu Lys
 660 665 670
 Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg Asn Gly Ser Asp
 675 680 685
 Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr Lys Asn Leu Leu
 690 695 700
 Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His Gly Lys Thr Thr
 705 710 715 720
 Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly Ile Thr Asn Leu
 725 730 735
 Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys Glu Phe Leu Arg
 740 745 750

Lys

<210> 7
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 <220>
 <223> Lactoferin / HFE-based recycling domain RC4
 <400> 7

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 <211> 21
 <212> PRT
 <213> Mus musculus

<400> 8

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
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Gly Ser Thr Gly Asp
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<210> 9
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 9

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

Asp Thr Thr Gly
 20

<210> 10
 <211> 301
 <212> PRT
 <213> Homo sapiens

<400> 10

Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln His Ile
 1 5 10 15

Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala
 20 25 30

His Lys Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu
 35 40 45

Ser Ile Thr Lys Ser Ala Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser
 50 55 60

Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn His Thr Gly Phe Tyr Ser
 65 70 75 80

Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser
 85 90 95

Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met

100	105	110
Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu 115 120 125		
Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys 130 135 140		
Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp 145 150 155 160		
Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile 165 170 175		
Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr 180 185 190		
Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile 195 200 205		
Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val Leu 210 215 220		
Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr Trp 225 230 235 240		
Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg Ile 245 250 255		
Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile 260 265 270		
Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg 275 280 285		
Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His 290 295 300		

<210> 11
 <211> 1042
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CFP-RC1(n) VEGF

<400> 11

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro 1 5 10 15
Gly Ser Thr Gly Asp Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser 20 25 30

Pro Ile Gln Cys Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val
 35 40 45
 Thr Leu Asp Gly Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys
 50 55 60
 Leu Arg Pro Val Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg
 65 70 75 80
 Thr His Tyr Tyr Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln
 85 90 95
 Leu Asn Glu Leu Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg
 100 105 110
 Thr Ala Gly Trp Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn
 115 120 125
 Trp Thr Gly Pro Pro Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe
 130 135 140
 Ser Ala Ser Cys Val Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu
 145 150 155 160
 Cys Arg Leu Cys Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser
 165 170 175
 Gln Glu Pro Tyr Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp
 180 185 190
 Gly Ala Gly Asp Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp
 195 200 205
 Leu Ser Asp Glu Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp
 210 215 220
 Asn Thr Arg Lys Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg
 225 230 235 240
 Val Pro Ser His Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp
 245 250 255
 Ala Ile Trp Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp
 260 265 270
 Lys Ser Pro Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp
 275 280 285
 Leu Leu Phe Lys Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg
 290 295 300
 Ile Asp Ser Gly Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln
 305 310 315 320
 Asn Leu Arg Lys Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val

	325		330		335	
Val Trp Cys	Ala Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp					
	340		345		350	
Ser Gly Leu	Ser Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr					
	355		360		365	
Glu Asp Cys	Ile Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser					
	370		375		380	
Leu Asp Gly	Gly Tyr Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro					
	385		390		395	400
Val Leu Ala	Glu Asn Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro					
		405		410		415
Asn Cys Val	Asp Arg Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val					
		420		425		430
Arg Arg Ser	Asp Thr Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys					
		435		440		445
Ser Cys His	Thr Ala Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met					
		450		455		460
Gly Leu Leu	Phe Asn Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe					
		465		470		475
Ser Gln Ser	Cys Ala Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala					
		485		490		495
Leu Cys Ile	Gly Asp Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser					
		500		505		510
Asn Glu Arg	Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu					
		515		520		525
Asn Ala Gly	Asp Val Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn					
		530		535		540
Thr Asp Gly	Asn Asn Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala					
		545		550		555
Asp Phe Ala	Leu Leu Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu					
		565		570		575
Ala Arg Ser	Cys His Leu Ala Met Ala Pro Asn His Ala Val Val Ser					
		580		585		590
Arg Met Asp	Lys Val Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln					
		595		600		605
Ala Lys Phe	Gly Arg Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu					
		610		615		620

Phe Gln Ser Glu Thr Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys
 625 630 635 640
 Leu Ala Arg Leu His Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro
 645 650 655
 Gln Tyr Val Ala Gly Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro
 660 665 670
 Leu Leu Glu Ala Cys Glu Phe Leu Arg Lys Val Pro Pro Leu Val Lys
 675 680 685
 Val Thr His His Val Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala
 690 695 700
 Leu Asn Tyr Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys
 705 710 715 720
 Gln Pro Met Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn
 725 730 735
 Gly Asp Gly Thr Tyr Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys
 740 745 750
 Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys
 755 760 765
 Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro Glu Met Val Ser Lys
 770 775 780
 Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala Cys Gly Arg Asn Gly
 785 790 795 800
 Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn His
 805 810 815
 Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys
 820 825 830
 Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg
 835 840 845
 Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr
 850 855 860
 Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile
 865 870 875 880
 Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly
 885 890 895
 Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala
 900 905 910

Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly
 915 920 925
 His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile
 930 935 940
 Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly
 945 950 955 960
 His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg
 965 970 975
 Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser
 980 985 990
 Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr
 995 1000 1005
 Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu
 1010 1015 1020
 Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn
 1025 1030 1035
 Thr Ser Val His
 1040

<210> 12
 <211> 597
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CFP-RC2(n) VEGF

<400> 12

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu
 20 25 30
 Phe Met Gly Ala Ser Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala
 35 40 45
 Leu Gly Tyr Val Asp Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser
 50 55 60
 Arg Arg Val Glu Pro Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser
 65 70 75 80
 Gln Met Trp Leu Gln Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met
 85 90 95

Phe Thr Val Asp Phe Trp Thr Ile Met Glu Asn His Asn His Ser Lys
 100 105 110
 Glu Ser His Thr Leu Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp
 115 120 125
 Asn Ser Thr Glu Gly Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His
 130 135 140
 Leu Glu Phe Cys Pro Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg
 145 150 155 160
 Ala Trp Pro Thr Lys Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg
 165 170 175
 Gln Asn Arg Ala Tyr Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln
 180 185 190
 Leu Leu Glu Leu Gly Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu
 195 200 205
 Val Lys Val Thr His His Val Thr Ser Ser Val Thr Thr Leu Arg Cys
 210 215 220
 Arg Ala Leu Asn Tyr Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys
 225 230 235 240
 Asp Lys Gln Pro Met Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu
 245 250 255
 Pro Asn Gly Asp Gly Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro
 260 265 270
 Pro Gly Glu Glu Gln Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu
 275 280 285
 Asp Gln Pro Leu Ile Val Ile Trp Ser Lys Leu Lys Asp Pro Glu Leu
 290 295 300
 Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr Leu His
 305 310 315 320
 Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro Glu Met
 325 330 335
 Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala Cys Gly
 340 345 350
 Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln
 355 360 365
 Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr
 370 375 380

Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp
 385 390 395 400
 Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile
 405 410 415
 His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser
 420 425 430
 Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile
 435 440 445
 Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile
 450 455 460
 Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr
 465 470 475 480
 Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr
 485 490 495
 Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu
 500 505 510
 Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu
 515 520 525
 Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys
 530 535 540
 Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His Ala Asn
 545 550 555 560
 Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys
 565 570 575
 Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val
 580 585 590
 Asn Thr Ser Val His
 595

<210> 13
 <211> 1042
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CFP-RC1(c) VEGF

<400> 13

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly Asp Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys
 20 25 30
 Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys
 35 40 45
 Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro Glu Met Val Ser Lys
 50 55 60
 Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala Cys Gly Arg Asn Gly
 65 70 75 80
 Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn His
 85 90 95
 Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys
 100 105 110
 Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg
 115 120 125
 Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr
 130 135 140
 Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile
 145 150 155 160
 Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly
 165 170 175
 Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala
 180 185 190
 Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly
 195 200 205
 His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile
 210 215 220
 Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly
 225 230 235 240
 His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg
 245 250 255
 Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser
 260 265 270
 Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr
 275 280 285
 Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr
 290 295 300

Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser
 305 310 315 320
 Val His Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln
 325 330 335
 Cys Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp
 340 345 350
 Gly Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro
 355 360 365
 Val Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr
 370 375 380
 Tyr Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu
 385 390 395 400
 Leu Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly
 405 410 415
 Trp Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly
 420 425 430
 Pro Pro Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser
 435 440 445
 Cys Val Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu
 450 455 460
 Cys Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro
 465 470 475 480
 Tyr Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly
 485 490 495
 Asp Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp
 500 505 510
 Glu Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg
 515 520 525
 Lys Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser
 530 535 540
 His Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp
 545 550 555 560
 Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro
 565 570 575
 Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe
 580 585 590
 Lys Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser

595					600					605					
Gly	Leu	Tyr	Leu	Gly	Ser	Gly	Tyr	Phe	Thr	Ala	Ile	Gln	Asn	Leu	Arg
610					615					620					
Lys	Ser	Glu	Glu	Glu	Val	Ala	Ala	Arg	Arg	Ala	Arg	Val	Val	Trp	Cys
625					630					635					640
Ala	Val	Gly	Glu	Gln	Glu	Leu	Arg	Lys	Cys	Asn	Gln	Trp	Ser	Gly	Leu
				645					650					655	
Ser	Glu	Gly	Ser	Val	Thr	Cys	Ser	Ser	Ala	Ser	Thr	Thr	Glu	Asp	Cys
			660					665					670		
Ile	Ala	Leu	Val	Leu	Lys	Gly	Glu	Ala	Asp	Ala	Met	Ser	Leu	Asp	Gly
		675					680					685			
Gly	Tyr	Val	Tyr	Thr	Ala	Gly	Lys	Cys	Gly	Leu	Val	Pro	Val	Leu	Ala
	690					695					700				
Glu	Asn	Tyr	Lys	Ser	Gln	Gln	Ser	Ser	Asp	Pro	Asp	Pro	Asn	Cys	Val
705					710					715					720
Asp	Arg	Pro	Val	Glu	Gly	Tyr	Leu	Ala	Val	Ala	Val	Val	Arg	Arg	Ser
				725					730					735	
Asp	Thr	Ser	Leu	Thr	Trp	Asn	Ser	Val	Lys	Gly	Lys	Lys	Ser	Cys	His
			740					745					750		
Thr	Ala	Val	Asp	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met	Gly	Leu	Leu
		755					760					765			
Phe	Asn	Gln	Thr	Gly	Ser	Cys	Lys	Phe	Asp	Glu	Tyr	Phe	Ser	Gln	Ser
	770					775					780				
Cys	Ala	Pro	Gly	Ser	Asp	Pro	Arg	Ser	Asn	Leu	Cys	Ala	Leu	Cys	Ile
785					790					795					800
Gly	Asp	Glu	Gln	Gly	Glu	Asn	Lys	Cys	Val	Pro	Asn	Ser	Asn	Glu	Arg
				805					810					815	
Tyr	Tyr	Gly	Tyr	Thr	Gly	Ala	Phe	Arg	Cys	Leu	Ala	Glu	Asn	Ala	Gly
			820					825					830		
Asp	Val	Ala	Phe	Val	Lys	Asp	Val	Thr	Val	Leu	Gln	Asn	Thr	Asp	Gly
		835					840					845			
Asn	Asn	Asn	Glu	Ala	Trp	Ala	Lys	Asp	Leu	Lys	Leu	Ala	Asp	Phe	Ala
		850				855					860				
Leu	Leu	Cys	Leu	Asp	Gly	Lys	Arg	Lys	Pro	Val	Thr	Glu	Ala	Arg	Ser
865					870					875					880
Cys	His	Leu	Ala	Met	Ala	Pro	Asn	His	Ala	Val	Val	Ser	Arg	Met	Asp
				885					890					895	

Lys Val Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe
 900 905 910
 Gly Arg Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser
 915 920 925
 Glu Thr Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg
 930 935 940
 Leu His Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val
 945 950 955 960
 Ala Gly Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu
 965 970 975
 Ala Cys Glu Phe Leu Arg Lys Val Pro Pro Leu Val Lys Val Thr His
 980 985 990
 His Val Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr
 995 1000 1005
 Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro
 1010 1015 1020
 Met Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly
 1025 1030 1035
 Asp Gly Thr Tyr
 1040

<210> 14
 <211> 597
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CFP-RC2(c)VEGF

<400> 14

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys
 20 25 30
 Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys
 35 40 45
 Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro Glu Met Val Ser Lys
 50 55 60
 Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala Cys Gly Arg Asn Gly

65		70		75		80									
Lys	Gln	Phe	Cys	Ser	Thr	Leu	Thr	Leu	Asn	Thr	Ala	Gln	Ala	Asn	His
			85					90						95	
Thr	Gly	Phe	Tyr	Ser	Cys	Lys	Tyr	Leu	Ala	Val	Pro	Thr	Ser	Lys	Lys
			100					105					110		
Lys	Glu	Thr	Glu	Ser	Ala	Ile	Tyr	Ile	Phe	Ile	Ser	Asp	Thr	Gly	Arg
		115					120					125			
Pro	Phe	Val	Glu	Met	Tyr	Ser	Glu	Ile	Pro	Glu	Ile	Ile	His	Met	Thr
	130					135					140				
Glu	Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val	Thr	Ser	Pro	Asn	Ile
145					150					155					160
Thr	Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr	Leu	Ile	Pro	Asp	Gly
				165					170					175	
Lys	Arg	Ile	Ile	Trp	Asp	Ser	Arg	Lys	Gly	Phe	Ile	Ile	Ser	Asn	Ala
		180						185					190		
Thr	Tyr	Lys	Glu	Ile	Gly	Leu	Leu	Thr	Cys	Glu	Ala	Thr	Val	Asn	Gly
		195					200						205		
His	Leu	Tyr	Lys	Thr	Asn	Tyr	Leu	Thr	His	Arg	Gln	Thr	Asn	Thr	Ile
	210					215					220				
Ile	Asp	Val	Gln	Ile	Ser	Thr	Pro	Arg	Pro	Val	Lys	Leu	Leu	Arg	Gly
225					230					235					240
His	Thr	Leu	Val	Leu	Asn	Cys	Thr	Ala	Thr	Thr	Pro	Leu	Asn	Thr	Arg
				245					250					255	
Val	Gln	Met	Thr	Trp	Ser	Tyr	Pro	Asp	Glu	Lys	Asn	Lys	Arg	Ala	Ser
		260						265					270		
Val	Arg	Arg	Arg	Ile	Asp	Gln	Ser	Asn	Ser	His	Ala	Asn	Ile	Phe	Tyr
		275					280					285			
Ser	Val	Leu	Thr	Ile	Asp	Lys	Met	Gln	Asn	Lys	Asp	Lys	Gly	Leu	Tyr
	290					295					300				
Thr	Cys	Arg	Val	Arg	Ser	Gly	Pro	Ser	Phe	Lys	Ser	Val	Asn	Thr	Ser
305					310					315					320
Val	His	Arg	Leu	Leu	Arg	Ser	His	Ser	Leu	His	Tyr	Leu	Phe	Met	Gly
				325					330					335	
Ala	Ser	Glu	Gln	Asp	Leu	Gly	Leu	Ser	Leu	Phe	Glu	Ala	Leu	Gly	Tyr
			340				345						350		
Val	Asp	Asp	Gln	Leu	Phe	Val	Phe	Tyr	Asp	His	Glu	Ser	Arg	Arg	Val
		355					360						365		

Glu Pro Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp
 370 375 380
 Leu Gln Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val
 385 390 395 400
 Asp Phe Trp Thr Ile Met Glu Asn His Asn His Ser Lys Glu Ser His
 405 410 415
 Thr Leu Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr
 420 425 430
 Glu Gly Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His Leu Glu Phe
 435 440 445
 Cys Pro Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro
 450 455 460
 Thr Lys Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg
 465 470 475 480
 Ala Tyr Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln Leu Leu Glu
 485 490 495
 Leu Gly Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu Val Lys Val
 500 505 510
 Thr His His Val Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu
 515 520 525
 Asn Tyr Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln
 530 535 540
 Pro Met Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly
 545 550 555 560
 Asp Gly Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu
 565 570 575
 Glu Gln Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro
 580 585 590
 Leu Ile Val Ile Trp
 595

<210> 15
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 15

Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser

1	5	10	15
Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys	20	25	30
Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser	35	40	45
Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys	50	55	60
Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp	65	70	75
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp	85	90	95
Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly	100	105	110
Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys	115	120	125
His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn	130	135	140
Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu	145	150	155
Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro Leu	165	170	175
Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu	180	185	190
Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val Cys	195	200	205
Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr Thr	210	215	220
Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr	225	230	235
Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser	245	250	

<210> 16
 <211> 992
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CFP-RC1(n)TNF

<400> 16

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser
 20 25 30
 Pro Ile Gln Cys Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val
 35 40 45
 Thr Leu Asp Gly Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys
 50 55 60
 Leu Arg Pro Val Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg
 65 70 75 80
 Thr His Tyr Tyr Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln
 85 90 95
 Leu Asn Glu Leu Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg
 100 105 110
 Thr Ala Gly Trp Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn
 115 120 125
 Trp Thr Gly Pro Pro Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe
 130 135 140
 Ser Ala Ser Cys Val Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu
 145 150 155 160
 Cys Arg Leu Cys Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser
 165 170 175
 Gln Glu Pro Tyr Phe Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp
 180 185 190
 Gly Ala Gly Asp Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp
 195 200 205
 Leu Ser Asp Glu Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp
 210 215 220
 Asn Thr Arg Lys Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg
 225 230 235 240
 Val Pro Ser His Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp
 245 250 255
 Ala Ile Trp Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp
 260 265 270
 Lys Ser Pro Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp

275					280					285					
Leu	Leu	Phe	Lys	Asp	Ser	Ala	Ile	Gly	Phe	Ser	Arg	Val	Pro	Pro	Arg
290					295					300					
Ile	Asp	Ser	Gly	Leu	Tyr	Leu	Gly	Ser	Gly	Tyr	Phe	Thr	Ala	Ile	Gln
305					310					315					320
Asn	Leu	Arg	Lys	Ser	Glu	Glu	Glu	Val	Ala	Ala	Arg	Arg	Ala	Arg	Val
				325					330					335	
Val	Trp	Cys	Ala	Val	Gly	Glu	Gln	Glu	Leu	Arg	Lys	Cys	Asn	Gln	Trp
			340					345					350		
Ser	Gly	Leu	Ser	Glu	Gly	Ser	Val	Thr	Cys	Ser	Ser	Ala	Ser	Thr	Thr
		355					360					365			
Glu	Asp	Cys	Ile	Ala	Leu	Val	Leu	Lys	Gly	Glu	Ala	Asp	Ala	Met	Ser
	370					375					380				
Leu	Asp	Gly	Gly	Tyr	Val	Tyr	Thr	Ala	Gly	Lys	Cys	Gly	Leu	Val	Pro
385					390					395					400
Val	Leu	Ala	Glu	Asn	Tyr	Lys	Ser	Gln	Gln	Ser	Ser	Asp	Pro	Asp	Pro
				405					410					415	
Asn	Cys	Val	Asp	Arg	Pro	Val	Glu	Gly	Tyr	Leu	Ala	Val	Ala	Val	Val
			420					425					430		
Arg	Arg	Ser	Asp	Thr	Ser	Leu	Thr	Trp	Asn	Ser	Val	Lys	Gly	Lys	Lys
		435					440					445			
Ser	Cys	His	Thr	Ala	Val	Asp	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met
	450					455					460				
Gly	Leu	Leu	Phe	Asn	Gln	Thr	Gly	Ser	Cys	Lys	Phe	Asp	Glu	Tyr	Phe
465					470					475					480
Ser	Gln	Ser	Cys	Ala	Pro	Gly	Ser	Asp	Pro	Arg	Ser	Asn	Leu	Cys	Ala
				485					490					495	
Leu	Cys	Ile	Gly	Asp	Glu	Gln	Gly	Glu	Asn	Lys	Cys	Val	Pro	Asn	Ser
			500					505					510		
Asn	Glu	Arg	Tyr	Tyr	Gly	Tyr	Thr	Gly	Ala	Phe	Arg	Cys	Leu	Ala	Glu
		515					520					525			
Asn	Ala	Gly	Asp	Val	Ala	Phe	Val	Lys	Asp	Val	Thr	Val	Leu	Gln	Asn
				530			535					540			
Thr	Asp	Gly	Asn	Asn	Asn	Glu	Ala	Trp	Ala	Lys	Asp	Leu	Lys	Leu	Ala
545					550					555					560
Asp	Phe	Ala	Leu	Leu	Cys	Leu	Asp	Gly	Lys	Arg	Lys	Pro	Val	Thr	Glu
				565					570					575	

Ala	Arg	Ser	Cys	His	Leu	Ala	Met	Ala	Pro	Asn	His	Ala	Val	Val	Ser	580	585	590
Arg	Met	Asp	Lys	Val	Glu	Arg	Leu	Lys	Gln	Val	Leu	Leu	His	Gln	Gln	595	600	605
Ala	Lys	Phe	Gly	Arg	Asn	Gly	Ser	Asp	Cys	Pro	Asp	Lys	Phe	Cys	Leu	610	615	620
Phe	Gln	Ser	Glu	Thr	Lys	Asn	Leu	Leu	Phe	Asn	Asp	Asn	Thr	Glu	Cys	625	630	635
Leu	Ala	Arg	Leu	His	Gly	Lys	Thr	Thr	Tyr	Glu	Lys	Tyr	Leu	Gly	Pro	645	650	655
Gln	Tyr	Val	Ala	Gly	Ile	Thr	Asn	Leu	Lys	Lys	Cys	Ser	Thr	Ser	Pro	660	665	670
Leu	Leu	Glu	Ala	Cys	Glu	Phe	Leu	Arg	Lys	Val	Pro	Pro	Leu	Val	Lys	675	680	685
Val	Thr	His	His	Val	Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala	690	695	700
Leu	Asn	Tyr	Tyr	Pro	Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys	705	710	715
Gln	Pro	Met	Asp	Ala	Lys	Glu	Phe	Glu	Pro	Lys	Asp	Val	Leu	Pro	Asn	725	730	735
Gly	Asp	Gly	Thr	Tyr	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	740	745	750
Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	755	760	765
Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	770	775	780
Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	785	790	795
Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	805	810	815
Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	820	825	830
Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	835	840	845
Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	850	855	860

Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys
865 870 875 880

Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
885 890 895

Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr
900 905 910

Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu
915 920 925

Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu
930 935 940

Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu
945 950 955 960

Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro
965 970 975

Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser
980 985 990

<210> 17

<211> 547

<212> PRT

<213> Artificial sequence

<220>

<223> CFP-RC2(n)TNF

<400> 17

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu
20 25 30

Phe Met Gly Ala Ser Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala
35 40 45

Leu Gly Tyr Val Asp Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser
50 55 60

Arg Arg Val Glu Pro Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser
65 70 75 80

Gln Met Trp Leu Gln Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met
85 90 95

Phe Thr Val Asp Phe Trp Thr Ile Met Glu Asn His Asn His Ser Lys
100 105 110

Glu Ser His Thr Leu Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp
 115 120 125
 Asn Ser Thr Glu Gly Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His
 130 135 140
 Leu Glu Phe Cys Pro Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg
 145 150 155 160
 Ala Trp Pro Thr Lys Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg
 165 170 175
 Gln Asn Arg Ala Tyr Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln
 180 185 190
 Leu Leu Glu Leu Gly Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu
 195 200 205
 Val Lys Val Thr His His Val Thr Ser Ser Val Thr Thr Leu Arg Cys
 210 215 220
 Arg Ala Leu Asn Tyr Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys
 225 230 235 240
 Asp Lys Gln Pro Met Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu
 245 250 255
 Pro Asn Gly Asp Gly Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro
 260 265 270
 Pro Gly Glu Glu Gln Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu
 275 280 285
 Asp Gln Pro Leu Ile Val Ile Trp Asp Ser Val Cys Pro Gln Gly Lys
 290 295 300
 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 305 310 315 320
 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
 325 330 335
 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
 340 345 350
 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
 355 360 365
 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
 370 375 380
 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
 385 390 395 400

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
 405 410 415
 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
 420 425 430
 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
 435 440 445
 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
 450 455 460
 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
 465 470 475 480
 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
 485 490 495
 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
 500 505 510
 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
 515 520 525
 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
 530 535 540
 Pro Ser Ser
 545

<210> 18
 <211> 992
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CFP-RC1(c)TNF

<400> 18

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His
 20 25 30
 Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr
 35 40 45
 Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu
 50 55 60
 Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys
 65 70 75 80

Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser
 85 90 95
 Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln
 100 105 110
 Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser
 115 120 125
 Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn
 130 135 140
 Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys
 145 150 155 160
 Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
 165 170 175
 Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr
 180 185 190
 Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu
 195 200 205
 Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu
 210 215 220
 Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu
 225 230 235 240
 Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro
 245 250 255
 Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser
 260 265 270
 Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile
 275 280 285
 Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly
 290 295 300
 Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala
 305 310 315 320
 Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala
 325 330 335
 Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln
 340 345 350
 Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn
 355 360 365

Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro
 370 375 380
 Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val
 385 390 395 400
 Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala
 405 410 415
 Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe
 420 425 430
 Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val
 435 440 445
 Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala
 450 455 460
 Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro
 465 470 475 480
 Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala
 485 490 495
 Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu
 500 505 510
 Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe
 515 520 525
 Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp
 530 535 540
 Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu
 545 550 555 560
 Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser
 565 570 575
 Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val
 580 585 590
 Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu
 595 600 605
 Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala
 610 615 620
 Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr
 625 630 635 640
 Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn
 645 650 655
 Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg

660	665	670
Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr 675 680 685		
Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala 690 695 700		
Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn 705 710 715 720		
Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala 725 730 735		
Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp 740 745 750		
Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr 755 760 765		
Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val 770 775 780		
Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn 785 790 795 800		
Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu 805 810 815		
Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His 820 825 830		
Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val 835 840 845		
Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg 850 855 860		
Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr 865 870 875 880		
Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His 885 890 895		
Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly 900 905 910		
Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys 915 920 925		
Glu Phe Leu Arg Lys Val Pro Pro Leu Val Lys Val Thr His His Val 930 935 940		
Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr Tyr Pro 945 950 955 960		

Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met Asp Ala
 965 970 975

Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly Thr Tyr
 980 985 990

<210> 19

<211> 547

<212> PRT

<213> Artificial sequence

<220>

<223> CFP-RC2(c)TNF

<400> 19

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly Asp Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His
 20 25 30

Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr
 35 40 45

Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu
 50 55 60

Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys
 65 70 75 80

Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser
 85 90 95

Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln
 100 105 110

Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser
 115 120 125

Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn
 130 135 140

Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys
 145 150 155 160

Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
 165 170 175

Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr
 180 185 190

Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu

195					200					205					
Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys	Ser	Lys	Leu
210						215					220				
Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys	Glu	Gly	Glu	Leu
225					230					235					240
Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn	Pro	Ser	Phe	Ser	Pro
				245					250					255	
Thr	Pro	Gly	Phe	Thr	Pro	Thr	Leu	Gly	Phe	Ser	Pro	Val	Pro	Ser	Ser
			260					265						270	
Arg	Leu	Leu	Arg	Ser	His	Ser	Leu	His	Tyr	Leu	Phe	Met	Gly	Ala	Ser
		275					280					285			
Glu	Gln	Asp	Leu	Gly	Leu	Ser	Leu	Phe	Glu	Ala	Leu	Gly	Tyr	Val	Asp
		290				295					300				
Asp	Gln	Leu	Phe	Val	Phe	Tyr	Asp	His	Glu	Ser	Arg	Arg	Val	Glu	Pro
305					310					315					320
Arg	Thr	Pro	Trp	Val	Ser	Ser	Arg	Ile	Ser	Ser	Gln	Met	Trp	Leu	Gln
				325					330					335	
Leu	Ser	Gln	Ser	Leu	Lys	Gly	Trp	Asp	His	Met	Phe	Thr	Val	Asp	Phe
			340					345					350		
Trp	Thr	Ile	Met	Glu	Asn	His	Asn	His	Ser	Lys	Glu	Ser	His	Thr	Leu
		355					360					365			
Gln	Val	Ile	Leu	Gly	Cys	Glu	Met	Gln	Glu	Asp	Asn	Ser	Thr	Glu	Gly
	370					375					380				
Tyr	Trp	Lys	Tyr	Gly	Tyr	Asp	Gly	Gln	Asp	His	Leu	Glu	Phe	Cys	Pro
385					390					395					400
Asp	Thr	Leu	Asp	Trp	Arg	Ala	Ala	Glu	Pro	Arg	Ala	Trp	Pro	Thr	Lys
				405					410					415	
Leu	Glu	Trp	Glu	Arg	His	Lys	Ile	Arg	Ala	Arg	Gln	Asn	Arg	Ala	Tyr
			420					425					430		
Leu	Glu	Arg	Asp	Cys	Pro	Ala	Gln	Leu	Gln	Gln	Leu	Leu	Glu	Leu	Gly
		435					440					445			
Arg	Gly	Val	Leu	Asp	Gln	Gln	Val	Pro	Pro	Leu	Val	Lys	Val	Thr	His
	450					455					460				
His	Val	Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala	Leu	Asn	Tyr
465					470					475					480
Tyr	Pro	Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys	Gln	Pro	Met
				485					490					495	

Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly
500 505 510

Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu Glu Gln
515 520 525

Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro Leu Ile
530 535 540

Val Ile Trp
545

<210> 20
<211> 169
<212> PRT
<213> Homo sapiens

<400> 20

Thr Pro Val Ser Gln Thr Thr Thr Ala Ala Thr Ala Ser Val Arg Ser
1 5 10 15

Thr Lys Asp Pro Cys Pro Ser Gln Pro Pro Val Phe Pro Ala Ala Lys
20 25 30

Gln Cys Pro Ala Leu Glu Val Thr Trp Pro Glu Val Glu Val Pro Leu
35 40 45

Asn Gly Thr Leu Ser Leu Ser Cys Val Ala Cys Ser Arg Phe Pro Asn
50 55 60

Phe Ser Ile Leu Tyr Trp Leu Gly Asn Gly Ser Phe Ile Glu His Leu
65 70 75 80

Pro Gly Arg Leu Trp Glu Gly Ser Thr Ser Arg Glu Arg Gly Ser Thr
85 90 95

Gly Thr Gln Leu Cys Lys Ala Leu Val Leu Glu Gln Leu Thr Pro Ala
100 105 110

Leu His Ser Thr Asn Phe Ser Cys Val Leu Val Asp Pro Glu Gln Val
115 120 125

Val Gln Arg His Val Val Leu Ala Gln Leu Trp Val Arg Ser Pro Arg
130 135 140

Arg Gly Leu Gln Glu Gln Glu Leu Cys Phe His Met Trp Gly Gly
145 150 155 160

Lys Gly Gly Leu Cys Gln Ser Ser Leu
165

<210> 21
 <211> 910
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CFP-RC1(n)IL18

<400> 21

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro	1	5	10	15
Gly	Ser	Thr	Gly	Asp	Gly	Pro	Pro	Val	Ser	Cys	Ile	Lys	Arg	Asp	Ser	20	25	30	
Pro	Ile	Gln	Cys	Ile	Gln	Ala	Ile	Ala	Glu	Asn	Arg	Ala	Asp	Ala	Val	35	40	45	
Thr	Leu	Asp	Gly	Gly	Phe	Ile	Tyr	Glu	Ala	Gly	Leu	Ala	Pro	Tyr	Lys	50	55	60	
Leu	Arg	Pro	Val	Ala	Ala	Glu	Val	Tyr	Gly	Thr	Glu	Arg	Gln	Pro	Arg	65	70	75	80
Thr	His	Tyr	Tyr	Ala	Val	Ala	Val	Val	Lys	Lys	Gly	Gly	Ser	Phe	Gln	85	90	95	
Leu	Asn	Glu	Leu	Gln	Gly	Leu	Lys	Ser	Cys	His	Thr	Gly	Leu	Arg	Arg	100	105	110	
Thr	Ala	Gly	Trp	Asn	Val	Pro	Ile	Gly	Thr	Leu	Arg	Pro	Phe	Leu	Asn	115	120	125	
Trp	Thr	Gly	Pro	Pro	Glu	Pro	Ile	Glu	Ala	Ala	Val	Ala	Arg	Phe	Phe	130	135	140	
Ser	Ala	Ser	Cys	Val	Pro	Gly	Ala	Asp	Lys	Gly	Gln	Phe	Pro	Asn	Leu	145	150	155	160
Cys	Arg	Leu	Cys	Ala	Gly	Thr	Gly	Glu	Asn	Lys	Cys	Ala	Phe	Ser	Ser	165	170	175	
Gln	Glu	Pro	Tyr	Phe	Ser	Tyr	Ser	Gly	Ala	Phe	Lys	Cys	Leu	Arg	Asp	180	185	190	
Gly	Ala	Gly	Asp	Val	Ala	Phe	Ile	Arg	Glu	Ser	Thr	Val	Phe	Glu	Asp	195	200	205	
Leu	Ser	Asp	Glu	Ala	Glu	Arg	Asp	Glu	Tyr	Glu	Leu	Leu	Cys	Pro	Asp	210	215	220	
Asn	Thr	Arg	Lys	Pro	Val	Asp	Lys	Phe	Lys	Asp	Cys	His	Leu	Ala	Arg	225	230	235	240

Val Pro Ser His Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp
 245 250 255
 Ala Ile Trp Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp
 260 265 270
 Lys Ser Pro Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp
 275 280 285
 Leu Leu Phe Lys Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg
 290 295 300
 Ile Asp Ser Gly Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln
 305 310 315 320
 Asn Leu Arg Lys Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val
 325 330 335
 Val Trp Cys Ala Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp
 340 345 350
 Ser Gly Leu Ser Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr
 355 360 365
 Glu Asp Cys Ile Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser
 370 375 380
 Leu Asp Gly Gly Tyr Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro
 385 390 395 400
 Val Leu Ala Glu Asn Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro
 405 410 415
 Asn Cys Val Asp Arg Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val
 420 425 430
 Arg Arg Ser Asp Thr Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys
 435 440 445
 Ser Cys His Thr Ala Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met
 450 455 460
 Gly Leu Leu Phe Asn Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe
 465 470 475 480
 Ser Gln Ser Cys Ala Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala
 485 490 495
 Leu Cys Ile Gly Asp Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser
 500 505 510
 Asn Glu Arg Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu
 515 520 525
 Asn Ala Gly Asp Val Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn

530				535				540							
Thr	Asp	Gly	Asn	Asn	Asn	Glu	Ala	Trp	Ala	Lys	Asp	Leu	Lys	Leu	Ala
545					550					555					560
Asp	Phe	Ala	Leu	Leu	Cys	Leu	Asp	Gly	Lys	Arg	Lys	Pro	Val	Thr	Glu
			565						570					575	
Ala	Arg	Ser	Cys	His	Leu	Ala	Met	Ala	Pro	Asn	His	Ala	Val	Val	Ser
			580						585				590		
Arg	Met	Asp	Lys	Val	Glu	Arg	Leu	Lys	Gln	Val	Leu	Leu	His	Gln	Gln
		595					600						605		
Ala	Lys	Phe	Gly	Arg	Asn	Gly	Ser	Asp	Cys	Pro	Asp	Lys	Phe	Cys	Leu
	610					615					620				
Phe	Gln	Ser	Glu	Thr	Lys	Asn	Leu	Leu	Phe	Asn	Asp	Asn	Thr	Glu	Cys
625					630					635					640
Leu	Ala	Arg	Leu	His	Gly	Lys	Thr	Thr	Tyr	Glu	Lys	Tyr	Leu	Gly	Pro
				645					650					655	
Gln	Tyr	Val	Ala	Gly	Ile	Thr	Asn	Leu	Lys	Lys	Cys	Ser	Thr	Ser	Pro
			660						665					670	
Leu	Leu	Glu	Ala	Cys	Glu	Phe	Leu	Arg	Lys	Val	Pro	Pro	Leu	Val	Lys
		675					680						685		
Val	Thr	His	His	Val	Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala
		690				695					700				
Leu	Asn	Tyr	Tyr	Pro	Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys
705					710					715					720
Gln	Pro	Met	Asp	Ala	Lys	Glu	Phe	Glu	Pro	Lys	Asp	Val	Leu	Pro	Asn
				725					730					735	
Gly	Asp	Gly	Thr	Tyr	Thr	Pro	Val	Ser	Gln	Thr	Thr	Thr	Ala	Ala	Thr
			740						745					750	
Ala	Ser	Val	Arg	Ser	Thr	Lys	Asp	Pro	Cys	Pro	Ser	Gln	Pro	Pro	Val
		755					760						765		
Phe	Pro	Ala	Ala	Lys	Gln	Cys	Pro	Ala	Leu	Glu	Val	Thr	Trp	Pro	Glu
		770				775					780				
Val	Glu	Val	Pro	Leu	Asn	Gly	Thr	Leu	Ser	Leu	Ser	Cys	Val	Ala	Cys
785					790					795					800
Ser	Arg	Phe	Pro	Asn	Phe	Ser	Ile	Leu	Tyr	Trp	Leu	Gly	Asn	Gly	Ser
				805					810					815	
Phe	Ile	Glu	His	Leu	Pro	Gly	Arg	Leu	Trp	Glu	Gly	Ser	Thr	Ser	Arg
			820						825					830	

Glu Arg Gly Ser Thr Gly Thr Gln Leu Cys Lys Ala Leu Val Leu Glu
 835 840 845
 Gln Leu Thr Pro Ala Leu His Ser Thr Asn Phe Ser Cys Val Leu Val
 850 855 860
 Asp Pro Glu Gln Val Val Gln Arg His Val Val Leu Ala Gln Leu Trp
 865 870 875 880
 Val Arg Ser Pro Arg Arg Gly Leu Gln Glu Gln Glu Glu Leu Cys Phe
 885 890 895
 His Met Trp Gly Gly Lys Gly Gly Leu Cys Gln Ser Ser Leu
 900 905 910

<210> 22
 <211> 465
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CFP-RC2(n) IL18

<400> 22

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu
 20 25 30
 Phe Met Gly Ala Ser Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala
 35 40 45
 Leu Gly Tyr Val Asp Asp Gln Leu Phe Val Phe Tyr Asp His Glu Ser
 50 55 60
 Arg Arg Val Glu Pro Arg Thr Pro Trp Val Ser Ser Arg Ile Ser Ser
 65 70 75 80
 Gln Met Trp Leu Gln Leu Ser Gln Ser Leu Lys Gly Trp Asp His Met
 85 90 95
 Phe Thr Val Asp Phe Trp Thr Ile Met Glu Asn His Asn His Ser Lys
 100 105 110
 Glu Ser His Thr Leu Gln Val Ile Leu Gly Cys Glu Met Gln Glu Asp
 115 120 125
 Asn Ser Thr Glu Gly Tyr Trp Lys Tyr Gly Tyr Asp Gly Gln Asp His
 130 135 140
 Leu Glu Phe Cys Pro Asp Thr Leu Asp Trp Arg Ala Ala Glu Pro Arg

145		150		155		160
Ala Trp Pro Thr	Lys Leu Glu Trp Glu Arg His Lys Ile Arg Ala Arg					
	165			170		175
Gln Asn Arg Ala Tyr Leu Glu Arg Asp Cys Pro Ala Gln Leu Gln Gln						
	180			185		190
Leu Leu Glu Leu Gly Arg Gly Val Leu Asp Gln Gln Val Pro Pro Leu						
	195			200		205
Val Lys Val Thr His His Val Thr Ser Ser Val Thr Thr Leu Arg Cys						
	210			215		220
Arg Ala Leu Asn Tyr Tyr Pro Gln Asn Ile Thr Met Lys Trp Leu Lys						
	225			230		240
Asp Lys Gln Pro Met Asp Ala Lys Glu Phe Glu Pro Lys Asp Val Leu						
	245			250		255
Pro Asn Gly Asp Gly Thr Tyr Gln Gly Trp Ile Thr Leu Ala Val Pro						
	260			265		270
Pro Gly Glu Glu Gln Arg Tyr Thr Cys Gln Val Glu His Pro Gly Leu						
	275			280		285
Asp Gln Pro Leu Ile Val Ile Trp Thr Pro Val Ser Gln Thr Thr Thr						
	290			295		300
Ala Ala Thr Ala Ser Val Arg Ser Thr Lys Asp Pro Cys Pro Ser Gln						
	305			310		315
Pro Pro Val Phe Pro Ala Ala Lys Gln Cys Pro Ala Leu Glu Val Thr						
	325			330		335
Trp Pro Glu Val Glu Val Pro Leu Asn Gly Thr Leu Ser Leu Ser Cys						
	340			345		350
Val Ala Cys Ser Arg Phe Pro Asn Phe Ser Ile Leu Tyr Trp Leu Gly						
	355			360		365
Asn Gly Ser Phe Ile Glu His Leu Pro Gly Arg Leu Trp Glu Gly Ser						
	370			375		380
Thr Ser Arg Glu Arg Gly Ser Thr Gly Thr Gln Leu Cys Lys Ala Leu						
	385			390		395
Val Leu Glu Gln Leu Thr Pro Ala Leu His Ser Thr Asn Phe Ser Cys						
	405			410		415
Val Leu Val Asp Pro Glu Gln Val Val Gln Arg His Val Val Leu Ala						
	420			425		430
Gln Leu Trp Val Arg Ser Pro Arg Arg Gly Leu Gln Glu Gln Glu Glu						
	435			440		445

Leu Cys Phe His Met Trp Gly Gly Lys Gly Gly Leu Cys Gln Ser Ser
 450 455 460

Leu
 465

<210> 23
 <211> 910
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CFP-RC1(c)IL18

<400> 23

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly Asp Thr Pro Val Ser Gln Thr Thr Thr Ala Ala Thr
 20 25 30

Ala Ser Val Arg Ser Thr Lys Asp Pro Cys Pro Ser Gln Pro Pro Val
 35 40 45

Phe Pro Ala Ala Lys Gln Cys Pro Ala Leu Glu Val Thr Trp Pro Glu
 50 55 60

Val Glu Val Pro Leu Asn Gly Thr Leu Ser Leu Ser Cys Val Ala Cys
 65 70 75 80

Ser Arg Phe Pro Asn Phe Ser Ile Leu Tyr Trp Leu Gly Asn Gly Ser
 85 90 95

Phe Ile Glu His Leu Pro Gly Arg Leu Trp Glu Gly Ser Thr Ser Arg
 100 105 110

Glu Arg Gly Ser Thr Gly Thr Gln Leu Cys Lys Ala Leu Val Leu Glu
 115 120 125

Gln Leu Thr Pro Ala Leu His Ser Thr Asn Phe Ser Cys Val Leu Val
 130 135 140

Asp Pro Glu Gln Val Val Gln Arg His Val Val Leu Ala Gln Leu Trp
 145 150 155 160

Val Arg Ser Pro Arg Arg Gly Leu Gln Glu Gln Glu Glu Leu Cys Phe
 165 170 175

His Met Trp Gly Gly Lys Gly Gly Leu Cys Gln Ser Ser Leu Gly Pro
 180 185 190

Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile Gln Ala

195					200					205						
Ile	Ala	Glu	Asn	Arg	Ala	Asp	Ala	Val	Thr	Leu	Asp	Gly	Gly	Phe	Ile	
210					215					220						
Tyr	Glu	Ala	Gly	Leu	Ala	Pro	Tyr	Lys	Leu	Arg	Pro	Val	Ala	Ala	Glu	
225					230					235					240	
Val	Tyr	Gly	Thr	Glu	Arg	Gln	Pro	Arg	Thr	His	Tyr	Tyr	Ala	Val	Ala	
				245					250					255		
Val	Val	Lys	Lys	Gly	Gly	Ser	Phe	Gln	Leu	Asn	Glu	Leu	Gln	Gly	Leu	
				260				265					270			
Lys	Ser	Cys	His	Thr	Gly	Leu	Arg	Arg	Thr	Ala	Gly	Trp	Asn	Val	Pro	
				275			280					285				
Ile	Gly	Thr	Leu	Arg	Pro	Phe	Leu	Asn	Trp	Thr	Gly	Pro	Pro	Glu	Pro	
				290		295				300						
Ile	Glu	Ala	Ala	Val	Ala	Arg	Phe	Phe	Ser	Ala	Ser	Cys	Val	Pro	Gly	
305					310					315					320	
Ala	Asp	Lys	Gly	Gln	Phe	Pro	Asn	Leu	Cys	Arg	Leu	Cys	Ala	Gly	Thr	
				325					330					335		
Gly	Glu	Asn	Lys	Cys	Ala	Phe	Ser	Ser	Gln	Glu	Pro	Tyr	Phe	Ser	Tyr	
				340				345					350			
Ser	Gly	Ala	Phe	Lys	Cys	Leu	Arg	Asp	Gly	Ala	Gly	Asp	Val	Ala	Phe	
				355			360					365				
Ile	Arg	Glu	Ser	Thr	Val	Phe	Glu	Asp	Leu	Ser	Asp	Glu	Ala	Glu	Arg	
				370		375				380						
Asp	Glu	Tyr	Glu	Leu	Leu	Cys	Pro	Asp	Asn	Thr	Arg	Lys	Pro	Val	Asp	
385					390					395					400	
Lys	Phe	Lys	Asp	Cys	His	Leu	Ala	Arg	Val	Pro	Ser	His	Ala	Val	Val	
				405					410					415		
Ala	Arg	Ser	Val	Asn	Gly	Lys	Glu	Asp	Ala	Ile	Trp	Asn	Leu	Leu	Arg	
				420				425					430			
Gln	Ala	Gln	Glu	Lys	Phe	Gly	Lys	Asp	Lys	Ser	Pro	Lys	Phe	Gln	Leu	
				435			440					445				
Phe	Gly	Ser	Pro	Ser	Gly	Gln	Lys	Asp	Leu	Leu	Phe	Lys	Asp	Ser	Ala	
				450		455				460						
Ile	Gly	Phe	Ser	Arg	Val	Pro	Pro	Arg	Ile	Asp	Ser	Gly	Leu	Tyr	Leu	
465					470					475					480	
Gly	Ser	Gly	Tyr	Phe	Thr	Ala	Ile	Gln	Asn	Leu	Arg	Lys	Ser	Glu	Glu	
				485				490						495		

Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val Gly Glu
 500 505 510
 Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu Gly Ser
 515 520 525
 Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala Leu Val
 530 535 540
 Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr Val Tyr
 545 550 555 560
 Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Lys
 565 570 575
 Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg Pro Val
 580 585 590
 Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr Ser Leu
 595 600 605
 Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala Val Asp
 610 615 620
 Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn Gln Thr
 625 630 635 640
 Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala Pro Gly
 645 650 655
 Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp Glu Gln
 660 665 670
 Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr Gly Tyr
 675 680 685
 Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val Ala Phe
 690 695 700
 Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn Asn Glu
 705 710 715 720
 Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu Cys Leu
 725 730 735
 Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His Leu Ala
 740 745 750
 Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val Glu Arg
 755 760 765
 Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg Asn Gly
 770 775 780

Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr Lys Asn
785 790 795 800

Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His Gly Lys
805 810 815

Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly Ile Thr
820 825 830

Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys Glu Phe
835 840 845

Leu Arg Lys Val Pro Pro Leu Val Lys Val Thr His His Val Thr Ser
850 855 860

Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr Tyr Pro Gln Asn
865 870 875 880

Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met Asp Ala Lys Glu
885 890 895

Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly Thr Tyr
900 905 910

<210> 24

<211> 465

<212> PRT

<213> Artificial sequence

<220>

<223> CFP-RC2(c)IL18

<400> 24

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Thr Pro Val Ser Gln Thr Thr Thr Ala Ala Thr
20 25 30

Ala Ser Val Arg Ser Thr Lys Asp Pro Cys Pro Ser Gln Pro Pro Val
35 40 45

Phe Pro Ala Ala Lys Gln Cys Pro Ala Leu Glu Val Thr Trp Pro Glu
50 55 60

Val Glu Val Pro Leu Asn Gly Thr Leu Ser Leu Ser Cys Val Ala Cys
65 70 75 80

Ser Arg Phe Pro Asn Phe Ser Ile Leu Tyr Trp Leu Gly Asn Gly Ser
85 90 95

Phe Ile Glu His Leu Pro Gly Arg Leu Trp Glu Gly Ser Thr Ser Arg
100 105 110

Glu Arg Gly Ser Thr Gly Thr Gln Leu Cys Lys Ala Leu Val Leu Glu
 115 120 125
 Gln Leu Thr Pro Ala Leu His Ser Thr Asn Phe Ser Cys Val Leu Val
 130 135 140
 Asp Pro Glu Gln Val Val Gln Arg His Val Val Leu Ala Gln Leu Trp
 145 150 155 160
 Val Arg Ser Pro Arg Arg Gly Leu Gln Glu Gln Glu Glu Leu Cys Phe
 165 170 175
 His Met Trp Gly Gly Lys Gly Gly Leu Cys Gln Ser Ser Leu Arg Leu
 180 185 190
 Leu Arg Ser His Ser Leu His Tyr Leu Phe Met Gly Ala Ser Glu Gln
 195 200 205
 Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp Asp Gln
 210 215 220
 Leu Phe Val Phe Tyr Asp His Glu Ser Arg Arg Val Glu Pro Arg Thr
 225 230 235 240
 Pro Trp Val Ser Ser Arg Ile Ser Ser Gln Met Trp Leu Gln Leu Ser
 245 250 255
 Gln Ser Leu Lys Gly Trp Asp His Met Phe Thr Val Asp Phe Trp Thr
 260 265 270
 Ile Met Glu Asn His Asn His Ser Lys Glu Ser His Thr Leu Gln Val
 275 280 285
 Ile Leu Gly Cys Glu Met Gln Glu Asp Asn Ser Thr Glu Gly Tyr Trp
 290 295 300
 Lys Tyr Gly Tyr Asp Gly Gln Asp His Leu Glu Phe Cys Pro Asp Thr
 305 310 315 320
 Leu Asp Trp Arg Ala Ala Glu Pro Arg Ala Trp Pro Thr Lys Leu Glu
 325 330 335
 Trp Glu Arg His Lys Ile Arg Ala Arg Gln Asn Arg Ala Tyr Leu Glu
 340 345 350
 Arg Asp Cys Pro Ala Gln Leu Gln Gln Leu Leu Glu Leu Gly Arg Gly
 355 360 365
 Val Leu Asp Gln Gln Val Pro Pro Leu Val Lys Val Thr His His Val
 370 375 380
 Thr Ser Ser Val Thr Thr Leu Arg Cys Arg Ala Leu Asn Tyr Tyr Pro
 385 390 395 400

Gln Asn Ile Thr Met Lys Trp Leu Lys Asp Lys Gln Pro Met Asp Ala
405 410 415

Lys Glu Phe Glu Pro Lys Asp Val Leu Pro Asn Gly Asp Gly Thr Tyr
420 425 430

Gln Gly Trp Ile Thr Leu Ala Val Pro Pro Gly Glu Glu Gln Arg Tyr
435 440 445

Thr Cys Gln Val Glu His Pro Gly Leu Asp Gln Pro Leu Ile Val Ile
450 455 460

Trp
465